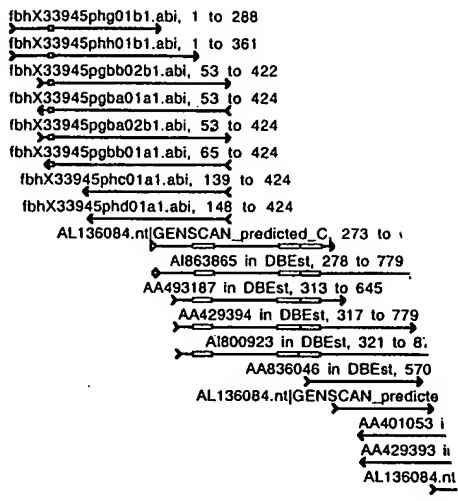


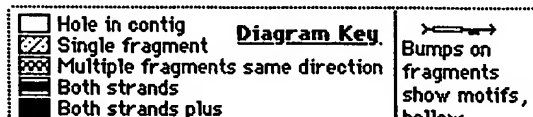
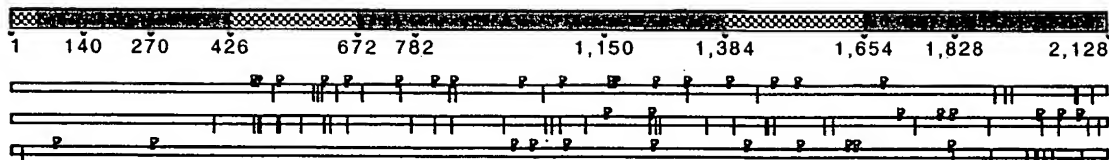
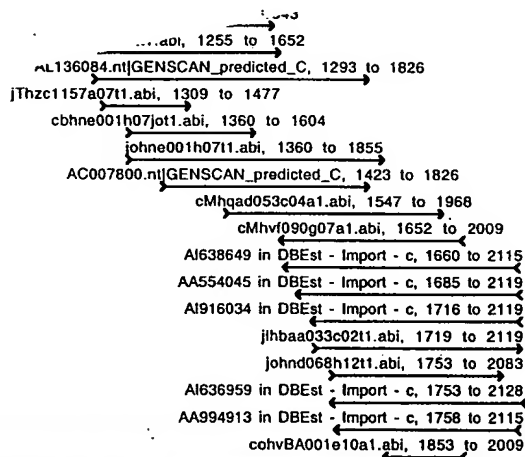
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Exhibit B1 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527

33945
Sequencher™ "33945"



*2 bp differences
that change amino acids
orthologs & genomic not
of great help. Decide
which to use - ph or pg.
Pete*



MI:fbhX33945pee03g1 (Human)**Description: Sample Information**

Name: fbhX33945pee03g1
Type: Full Length cDNA
Submitted on: Dec 12, 2000
NC project: Bayer
Species: Human
Tissue: unspecified
Internal id: 107050574

Sequence Information

Creation method: PhredBaseCall
Name: PHRED Base Calling Event
Created on: Dec 14, 2000
Created by: Pipeline
Accession number: (none)

Creation method: ABIBaseCall
Name: ABI Base Calling Event
Created on: Dec 14, 2000
Created by: Pipeline
Accession number: 107241068

Analyses: Note: Excludes periodic reanalysis events.

Description	Date	Requested by	Sta
<u>Internal Db Check</u>	Dec 14, 2000	Pipeline	YE
<u>CUR Mildb Check</u>	Dec 15, 2000	Pipeline	YE
<u>Nucleic Acid Db Check</u>	Dec 16, 2000	Pipeline	YE
<u>Protein Db Check</u>	Dec 16, 2000	Pipeline	YE
<u>DBEST Db Check</u>	Dec 16, 2000	Pipeline	YE
<u>PDB Db Check</u>	Dec 16, 2000	Pipeline	YE
<u>Signal Peptide Check</u>	Dec 16, 2000	Pipeline	YE
<u>1.4 BLAST vs. PNU</u>	May 28, 2004	Olga Tayber	SU
<u>1.4 BLAST vs. NUC</u>	May 28, 2004	Olga Tayber	SU

Base Array: **PHRED Base Call - complete**

Color and case key: NORMAL, low quality, vector, repeat

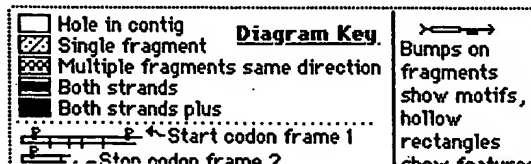
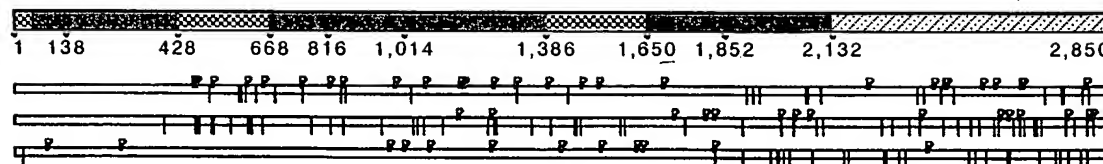
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TCCTGGCGCTACTGGCGTTGGCCGGGCTGGGCTCGGTGCTGCGGGCGCAGCGTGGGGCCG
GGGCCGGGCTGCCGAGCCGGGACCCCGCGCACCCCGCGCCCCGGGCGGCGGAGCCGG

TCATGCCGCGGCCGCCGGTGCCGGCGAACGCGCTGGGCGCGCGGGGCGAGGCGGTGCGGC
TGCAGCTGCAGGGCGAGGAGCTGCGGCTGCAGGAGGAGAGCGTGCGGCTGCACCAGATTA
ACATCTACCTCAGCGACCGCATCTCACTGCACCGgggctagagcgccgccaccgcggtg
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Comments:	Author	Date	Comment
<div></div>	<div></div>	<div></div>	<div></div>

33945
Sequencher™ "33945"

Exhibit B3 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527



Sample Information

name: Fbh33945FL
type: Plain DNA Sequence
submitted on: December 18 2000
NC project: Bayer
species: Human
tissue: unspecified
internal id: 107445732
restrictions: none

**Exhibit B4 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527**

Sequences Information

creation method: Loading
name: Load
created on: December 18 2000
created by: Peter Olandt
accession number: 107445733

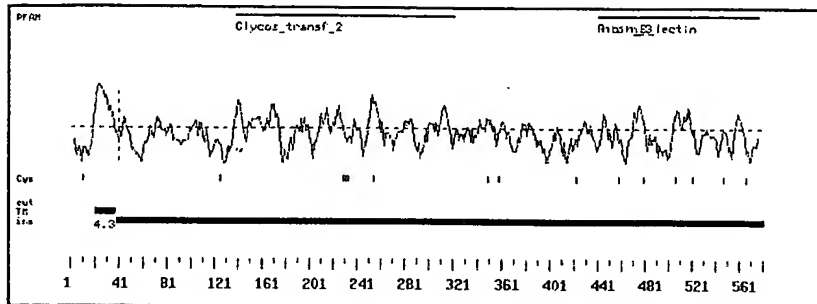
> Fbh33945FL - Import - complete

```
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61     TGGCTGCAGT TGGCGGGCGC ATGTGGGGGC GCACGGCGCG GCGGCGCTGC CCGCGGGAAC
121    TGGCGGCGCG CCGGGAGGCG CTGTTGGTGC TCCTGGCGCT ACTGGCGTTG GCCGGGCTGG
181    GCTCGGTGCT GCGGGCGCAG CGTGGGGCCG GGGCCGGGGC TGCCGAGCCG GGACCCCGCG
241    GCACCCCGCG CCCCGGGCGG CCGGAGCCGG TCATGCCCGG GCCGCCGGTG CCGGCGAACG
301    CGCTGGGCGC GCGGGGCGAG GCGGTGCGGC TGCAGCTGCA GGGCGAGGAG CTGCGGCTGC
361    AGGAGGAGAG CGTGCGGCTG CACCAGATTA ACATCTACCT CAGCGACCGC ATCTCACTGC
421    ACCGCCGCCT GCCCGAGCGC TGAACCCGCG TGTGCAAAGA GAAGAAATAT GATTATGATA
481    ATTTGCCCAG GACATCTGTT ATCATAGCAT TTTATAATGA AGCCTGGTCA ACTCTCCTTC
541    GGACAGTTTA CAGTGTCTTT GAGACATCCC CGGATATCCT GCTAGAAGAA GTGATCCTTG
601    TAGATGACTA CAGTGATAGA GAGCACCTGA AGGAGCGCTT GGCCAATGAG CTTTCGGGAC
661    TGCCCAAGGT GCGCCTGATC CGCGCCAACA AGAGAGAGGG CCTGGTGCGA GCGCGGCTGC
721    TGGGGGCGTC TGGGCGGAGG GCGGATGTTT TGACCTTCCT GGAAGTGCAC TGTGAGTGCC
781    ACGAAGGGTG GCTGGAGCCG CTGCTGCAGA GGATCCATGA AGAGGAGTCG GCAGTGGTGT
841    GCGCGGTGAT TGATGTGATC GACTGGAACA CCTTCGAATA CCTGGGGAAC TCCGGGGAGC
901    CCCAGATCGG CGGTTTCGAC TGGAGGCTGG TGTTCACGTG GCACACAGTT CTTGAGAGGG
961    AGAGGATACG GATGCAATCC CCCGTCGATG TCATCAGGTC TCCAACAATG GCTGGTGGGC
1021   TGTTTGCTGT GAGTAAGAAA TATTTTGAAT ATCTGGGGTC TTATGATACA GGAATGGAAG
1081   TTTGGGGAGG AGAAAACCTC GAATTTTCCT TTAGGATCTG GCAGTGTGGT GGGGTTCTGG
1141   AAACACACCC ATGTTCCCAT GTTGGCCATG TTTTCCCAA GCAAGCTCCC TACTCCCGCA
1201   ACAAGGCTCT GGCCAACAGT GTTCGTGCAG CTGAAGTATG GATGGATGAA TTAAAGAGC
1261   TCTACTACCA TCGCAACCCC CGTGCCCGCT TGGAACCTTT TGGGGATGTG ACAGAGAGGA
1321   AGCAGCTCCG GGACAAGCTC CAGTGTAAG ACTTCAAGTG GTTCTTGAG ACTGTGTATC
1381   CAGAACTGCA TGTGCCTGAG GACAGGCCTG GCTTCTCGG GATGCTCCAG AACAAAGGAC
1441   TAACAGACTA CTGCTTTGAC TATAACCTC CCGATGAAAA CCAGATTGTG GGACACCAGG
1501   TCATTCTGTA CCTCTGTGAT GGGATGGGCC AGAATCAGTT TTCGAGTAC ACGTCCCAGA
```

1561 AAGAAATACG CTATAACACC CACCAGCCTG AGGGCTGCGT TGCTGTGGAA GCAGGAATGG
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1741 AGTCGAGTGA CAGTTTCGTT CCACTCTTAC GAGACTGCAC CAACTCGGAT CATCAGAAAT
1801 GGTTCTTCAA AGAGCGCATG TTATGAAGCC TCGTGTATCA AGGAGCCCAT CGAAGGAGAC
1861 TGTGGAGCCA GGACTCTGCC CAACAAAGAC TTAGCTAAGC AGTGACCAGA ACCCACCAAA
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2101 CTTATAATAT TTTTCTATCA ARAWRWAWAT TTTACAGTCG TGCCTTTTAC TCTCATTAGC
2161 AAAAAAGATA AAGATTTTAT TTTGGTATTT ACAAGAATTC CCAGGTACGA AGATATCTGC
2221 ATGGGTGGAA ATCAGGTTC AAGCAACGTAC TTTGCATTAA CTGATAATAC CTCAGCTGCG
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2401 CACAGTTAAC ACTCCATAAT GTTCATGTCA GCCAAAGAGG ACTAACCAAA GCTGAAATCT
2461 CAGAGAACAA TTTGCTTTAC TAAGCTGAGT CAACTTGAGA GCGAACTTCT AACAAATGCCG
2521 CACTGTAGTG TGGCTGGTTC TACCACATG ACTTTAAAAC ATGTTTATAT CATTTTTAAT
2581 TTTTATGATA CGGTAGTGTC AGGGAGAAAT GTAATGTTCT ATATGAAATT CCTTTTCAA
2641 GTTTGTTTAT TAATAACAGT TATTAATTTA AATCAGCGTT AGAGTTTGTG CTGCTGCAAC
2701 TGCTGTGAAA ATTTCTCTGA GTAATTCTGA TTTGTGAATG ATCCCAGACC AACCCTGAGA
2761 TTTTGTCAAC CTGATTAAAGT CAATATGAAT GATTAAAAAG ATGTGAGAAC AAAAAA
2821 AAAAAA AAAAAA AAAAAA

[Back to orfanal.cgi](#)

Analysis of 33945 (581 aa)



>33945
 MKGRTARRRCPRELRGREALLVLLALLAGLSVLRAGAGAGAAEPFPTPRGR
 REPVMPPFPVPAALGARGAVRLQGEELRLQESVRLHQINILSDRISLHRLPER
 WNPCKEKKYDYNLPRTSVIIAFYNEAMSTLLRTVYSVLETSFDILLLEEVILVDDYSDR
 EHLKERLANELSGLPKVRILIRANKREGVLRLGASAAARGDVLTFDCHCECHGNLEP
 LLQRIHEESAVVCPVIDVIDMNTFFYLGNSGEPQIGFDMRLVFTMTVPERERIRHQ
 PVDVIRSPHAGLFAVSKKYPYLYGSDYDNEVMGDNLEFSFRIMCGGVLETHPCSH
 VGRVTFQGAIFYERKALANVRAAEVWDFEKLTYHNPRALEFPDPTERKQLRDL
 QCKDFKNTLETVPYELRVPEDRPGFCHLQNGKLTQYCFDYPDPDENIYGHQVILYLCN
 GGGQHPFFETTSQKEIRYNTHQPEGCIAYAGDGLILHLCEETAPENQKFLQEDGSLF
 HDQSKKCVQAARKESDSFVPLLRDCTNSHQHFFKERGL

PSORT Prediction of Protein Localization

MITDISC: discrimination of mitochondrial targeting seq
 A content: 8 Hyd Moment(75): 13.73
 Hyd Moment(95): 16.65 G content: 2
 D/E content: 2 S/T content: 1
 Score: 1.89

Gavel: prediction of cleavage sites for mitochondrial preseq
 R-2 motif at 19 RRC|PR

NUCDISC: discrimination of nuclear localization signals
 pat4: none
 pat7: PLCKEKK (3) at 123
 bipartite: none
 content of basic residues: 12.9%
 NLS Score: -0.22

ER Membrane Retention Signals:
 XXRR-like motif in the N-terminus: WGRT

KKKX-like motif in the C-terminus: KERM

Final Results (k = 9/23):

43.5 %: mitochondrial
 30.4 %: cytoplasmic
 8.7 %: vacuolar
 8.7 %: nuclear
 4.3 %: Golgi
 4.3 %: endoplasmic reticulum

prediction for 33945 in mit (k=23)

Start	End	Feature	Seq
86	107	Leucine zipper pattern (PS00029)	LQGEELRLQE...VRLHQINYL

Signal Peptide Predictions for 33945

Method	Predict	Score	Mat@
SignalP (eukaryote)	YES		40

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
20	37	out->ins	4.3

>33945
 MKGRTARRRCPRELRGREALLVLLALLAGLSVLRAGAGAGAAEPFPTPRGR
 REPVMPPFPVPAALGARGAVRLQGEELRLQESVRLHQINILSDRISLHRLPER
 WNPCKEKKYDYNLPRTSVIIAFYNEAMSTLLRTVYSVLETSFDILLLEEVILVDDYSDR
 EHLKERLANELSGLPKVRILIRANKREGVLRLGASAAARGDVLTFDCHCECHGNLEP

http://range.mpi.com/seqs/Verleno/33945_200208.html

LLQRIHEESAIVKPIVDIDWNTFEYLQNSCEPQIGFDMRLVFTWHTVPERERIKQGS
PVQVIRSPTHAGCLFAVSKRYFEYLGSYDTGHEVWGDHLEFSFRIWCCGVLETHPCSH
VGHVFKQAFYSRKAJANSVRAAEVNMDEFKELYHNRPRARLEPPQDUTERKQLRDKL
QCKDFDMFLETVPFELHVPEDRPGFFQMLQNKGLTYHCFDYNPPDENQIVGHQVILYLCH
GHGQHQFFETTSQKEIRYNTHQPECCI AVEAGHDTLIMHLCEETAPEHQKFLQEDGSLP
HDSKMCVQAARAESSDSFVPLLRUCTNSDHQWFFKERHL

Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
-------	-----	--------	-------

Prosite Pattern Matches for 33945

Prosite version: Release 12.2 of February 1995

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 552 RKES 555

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 5 TAR 7

Query: 55 TPR 57

Query: 97 SVR 99

Query: 108 SDR 110

Query: 178 SDR 180

Query: 318 SKK 320

Query: 343 SFR 345

Query: 380 SVR 382

Query: 411 TER 413

Query: 492 SQK 494

Query: 544 SKK 546

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 158 SVLE 161

Query: 162 TSPD 165

Query: 178 SDRE 181

Query: 225 TPLD 228

Query: 289 TVPE 292

Query: 300 SPVD 303

Query: 330 TGHE 333

Query: 492 SQKE 495

Query: 524 TAPE 527

Query: 567 TNSD 570

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 426 KWFLETYY 433

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 42 GAGAGA 47

Query: 207 GLVRAR 212

Query: 215 GASAAAR 220

Query: 312 GGLFAV 317

Query: 326 GSYDTG 331

Query: 351 GVLETH 356

Query: 447 GMLQNK 452

Query: 481 GHGQHQ 486




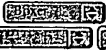

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 58 PGRR 61

>PS00010|PDOC00010|RGD Cell attachment sequence.

Query: 220 RGD 222

ProDom Matches

ProdomId	Start	End	Description	Score
View Prodom 2681 	101	138	p99.2 (20) PAGT(3) // TRANSFERASE N-ACETYL GALACTOSAMINYLTRANSFERASE POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N-	99
View Prodom 137344 	108	187	p99.2 (1) O44164_CAEEL // COSMID F16B3	74
View Prodom 93 	139	285	p99.2 (314) NODC(8) PAGT(3) CAG2(3) // PROTEIN TRANSFERASE GLYCOSYLTRANSFERASE PUTATIVE BIOSYNTHESIS GLYCOSYL SYNTHASE TRANSMEMBRANE N-ACETYL GALACTOSAMINYLTRANSFERASE MEMBRANE	108
View Prodom 2308 	287	443	p99.2 (23) PAGT(3) // N-ACETYL GALACTOSAMINYLTRANSFERASE TRANSFERASE POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N-	566
View Prodom 617 	453	574	p99.2 (70) PAGT(3) ABFB(2) E13B(2) // SIGNAL HYDROLASE PRECURSOR TOXIN RRNA N-GLYCOSIDASE GLYCOSIDASE LECTIN REPEAT GLYCOPROTEIN	104
ProdomId	Start	End	Description	Score

View Prodom 2308   

>2308 p99.2 (23) PAGT(3) // N-ACETYL GALACTOSAMINYLTRANSFERASE TRANSFERASE
POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N-
Length = 172

Score = 566 (204.3 bits), Expect = 3.3e-55, P = 3.3e-55
Identities = 102/166 (61%), Positives = 128/166 (77%)

Query: 287 MHTVPERERIRHQS-PVDVIRSPTHAGGLFAVSKKYFYLGSYDTCHVWGGDLELFSR 345
MH VPE ER R + P D IRSPTHAGGLFA+K+YFE LG+YD CH+MGGDLE SFR
Sbjct: 2 MHTVPEERKRRUKDPTDFIRSPTHAGGLFAINKEYFEELGTYDPCMDMGGENLELFSR 61

Query: 346 IMQCGVLETHPCERVCHVFPQAPYS-----RNKALANSVRAAEVWDEFKELYIHR 398
+MQCG LE PCSHVGRT K+VF+ ** N+VR AEVWD+EE Y
Sbjct: 62 VMQCGRLIVPCSHVGHVFKRSPYTFPGKSGKDVISRTVRAEVWDEYKYFYKH 121

Query: 399 NPAR-LEPPGVTERKQLRDKLOCKDFKMFLETVPYELHVPEDRP 443
NPAR + PGD+ERK+LR+KLQCK FKM+LE YIP+L+VP P
Sbjct: 122 NPQARVVDPGDISERKELRKLQCKSPKNYLENVYDLYVFAHEP 167

View Prodom 617 

>617 p99.2 (70) PAGT(3) ABFB(2) E13B(2) // SIGNAL HYDROLASE PRECURSOR TOXIN
RRNA N-GLYCOSIDASE GLYCOSIDASE LECTIN REPEAT GLYCOPROTEIN
Length = 140

Score = 104 (41.7 bits), Expect = 3.1e-05, P = 3.1e-05
Identities = 29/128 (22%), Positives = 55/128 (42%)

Query: 453 GLTDYCFDYNPPDENQVGHQVILYLCHQM-CQNOFFEYTSQKEIRYNHQPDCIAVEA 511
G C D N + + G+V L+ CH G NQ + + + IR N + + + C+
Sbjct: 11 GNNKGKLOVDNDRNTYLDGNFVOLMOCIRNKGQNTFNTDGTIRSKNKKX-CLTSSG 69

Query: 512 ----GNDTLIMHLCEETAPENKRFILOQDGLFHE-OSKKGVOAARKESSDFVPLRDC 566
G +I + MGR+ DG+ S C+ R +++ + C
Sbjct: 70 YSPVGSVMVYNCHSAKNDNQKMFNSDOTIIONPHSLCLDAYSMTANGTKIMVYTC 129

Query: 567 TNSDHOKW 574
+ + O+W
Sbjct: 130 MGNNSQOM 137

View Prodom 2681

>2681 p99.2 (20) PAGT(3) // TRANSFERASE N-ACETYL GALACTOSAMINYLTRANSFERASE
POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN- UDP N-
Length = 118

Score = 99 (39.9 bits), Expect = 0.00011, P = 0.00011
Identities = 21/39 (53%), Positives = 27/39 (69%)

Query: 101 NQFNLYSDRISLHRLPENNPLCKEKYD-YDNLPT 138
+O N+Y SD ISL+R LP+ CK +KY+ YDNL P
Sbjct: 80 NQFNLYASDMIASRLPDVPRPECKTKYNFYDNLPTT 118

View Prodom 93   

>93 p99.2 (314) NODC(8) FAGT(3) CAG2(3) // PROTEIN TRANSFERASE
GLYCOSYLTRANSFERASE PUTATIVE BIOSYNTHESIS GLYCOSYL SYNTHASE TRANSMEMBRANE
N-ACETYLGLALACTOSAMINYLTTRANSFERASE MEMBRANE
Length = 196

Score = 108 (43.1 bits), Expect = 0.00056, P = 0.00056
Identities = 46/163 (28%), Positives = 74/163 (45%)

Query: 139 SVIIAFYNAMSTLLRTVYVLETSPD--ILLEEVILVDDYS-DR--EHLKE-RLANELS 192
SVII YNE S L V SVL+ + +EE+VDD S D E +E + E
Sbjct: 3 SVIIPTYNNEESILKTLVSSVLQQYDHHYEMEEIIIVDDOSTNTAEIIVEEYSYSAKE 62

Query: 193 GLPKVRLIRANKREXXXXX-----XXXXXXXXXXDLTFLOCHCECHG--WLEPLQ 243
KV++IR K + + + D + FLO + M WLE L++
Sbjct: 63 SRVKVKVIRNEKNSGMSAHSKGLKHALSGADQDIIDYIVFLDSD-DVHHSPOWLEKLE 121

Query: 244 RIHEESAVVCPVIDIDMHTFEYLGNSGEPOI--GQFDMRLVF 285
+ E+ + WV V++ + +Y + + GQ++W +++
Sbjct: 122 AMEENADVVGSQVVDENKQYSSATRLIHMEGQYNSHNY 164

View Prodom 137344   

>137344 p99.2 (1) 044164_CAEEL // COSMID F1683
Length = 196

Score = 74 (31.1 bits), Expect = 4.9, P = 0.99
Identities = 23/80 (28%), Positives = 41/80 (51%)

Query: 108 SDRISLRRLPERNNPLCKKKYDYDNLPRTSVIIAFYNAMSTLLRTVYVLETSPDIL 167
S + R P+R PL R + D D L RTS + + NS+L + + + + DI+
Sbjct: 8 SSTVKSFRSKPKR-PPLAGQTVDEALSRTSNGCHKDKWSSL-SHRTKSKFDII 65

Query: 168 LEEVILVDDYSDEHLKERL 187
E + + + + R L ER+
Sbjct: 66 GERLTIEDQINSRLALLERV 85

Docket No. MPI01-018P1RNM

U.S. Serial No. 10/074,527, Filed February 12, 2002

EXHIBITS I – III

Exhibit I: U.S. Provisional Application No. 60/254,308, filed December 8, 2000,
by Sanjanwala et al. (entire file history document)

Exhibit II U.S. Provisional Application No. 60/256,189, filed December 15, 2000,
by Ding et al. (entire file history document)

Exhibit III U.S. Provisional Application No. 60/203,331, filed May 11, 2000,
by Hassen et al. (entire file history document)

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